**UNIVERSITY OF CAPE TOWN COMPUTATIONAL BIOLOGY DIVISION**

**Bioinformatics Support Request**

Please provide us with more information on your request for support. Complete the form as comprehensively as possible, and please indicate where there is still uncertainty.

**Please note, the earlier we are involved the better – for example, it would be better for us to be involved during the study design and even grant application stage**.

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| **CONTACT DETAILS** | |
| Date of request | **19-05-2020** |
| Name | **Sonwabile Dzanibe** |
| Email address | **sonwabile.dzanibe@uct.ac.za** |
| Research Group/Department | **IDM – Department of Pathology, Div. Immunology** |
| Faculty | **Health Sciences** |
| IF student, name & email of supervisor | **Clive Gray**  **Clive.gray@uct.ac.za** |

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| **PROJECT DETAILS** |
| 1. What is the scientific question? |
| The goal of the work is to determine transcriptomic differences in sorted Treg cells between infants who are HIV-exposed uninfected and HIV-unexposed uninfected. |
| 2. Who are the partners on the project? |
| This work is funded by SA-MRC self-initiated grant research. |
| 3. What type of collaboration with CBIO is expected? For a project that is done as collaboration or for a fee, we will put the agreement in writing. |
| Bioinformatic collaboration |
| 4. Are there any ethical issues we should be aware of? |
| No |
| 5. How much work is expected from CBIO and when? |
| Pipeline development for RNA seq data analysis.  As soon as convenient. |
| 6. What type of data will be generated (e.g. sequencing, genotyping, expression, etc.) and what technology platform will be used? |
| RNA seq data using Illumina platform |
| 7. When do you expect the data? Does it need to be transferred from somewhere else? |
| Data is available in the form of compressed fastq files |
| 8. How large will the data be? How long does it need to stored for, and have you made arrangements for storage? |
| Approximately 600 GB after unzipping the files. Files are to be uploaded onto the UCT G-drive. |
| 9. What bioinformatics analysis needs to be done? Which tools are required? |
| Standard RNA sequencing analysis including quality assessment, data normalization, alignment, gene mapping, pairwise comparisons, functional enrichment and visualization. |
| 10. If a collaborative model is being used, what papers are envisaged and who will the authors be? |
| Data from this analysis will be incorporated in a manuscript phenotyping the changes in immune cells (T regulatory and Th17 cells) during infancy or as a stand-alone manuscript. The authors will include the team in the Clive Gray and Heather Jaspan group involved in this work together with the Bioinfomatician from CBIO who is willing to collaborate with this analysis. |
| 11. Can we add a short description and objective of the project to the CBIO website? |
| Yes |

**PLEASE FORWARD THE COMPLETED FORM TO:**

[Nicola.mulder@uct.ac.za](mailto:Nicola.mulder@uct.ac.za)